

FORM PTO-1449

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54318.8001.USC

SERIAL NO.

09/905,176

LIST OF PATENTS AND OTHER ITEMS FOR APPLICANT'S
INFORMATION DISCLOSURE STATEMENT

APPLICANT:

DEBE, Derek A.

FILING DATE:

July 12, 2001

GROUP:

1645

(Use several sheets if necessary)

U.S. PATENT DOCUMENTS

EXAMINER R INITIAL	DOCUMENT NUMBER	DATE	NAME	CLASS	SUB CLASS	FILING DATE
AA						
AB						
AC						
AD						
AE						
AF						
AG						
AH						

RECEIVED

NOV 22 2002

TECH CENTER 1600/2900

FOREIGN PATENT DOCUMENTS

EXAMINER R INITIAL	DOCUMENT NUMBER	DATE	COUNTRY	CLASS	SUB CLASS	TRANSLATION YES NO
AI						
AJ						
AK						

OTHER DOCUMENTS (Including Author, Title, Date, Pertinent Pages, etc.)

ms	AL	Altschul, F., et al., "Basic Local Alignment Search Tool", J. Mol. Biol., Vol. 215 (1990), pp. 403-410
	AM	Altschul, F., et al., "Gapped BLAST and PSI-BLAST: A new generation of protein database search programs", Nuc. Acids Res., Vol. 25, No. 17 (1997), pp. 3389-3402
	AN	Aszódi, A., et al. "Homology modelling by distance geometry", Folding & Design Struct., Vol. 1 (1996), pp. 325-334
	AO	Berman, H., et al., "The Protein Data Bank", Nuc. Acids Res., Vol. 28, No. 1 (2000), pp. 235-242
	AP	Bernstein, F.C., et al., "The Protein Data Bank: A Computer-based Archival File for Macromolecular Structures", J. Mol. Biol., Vol. 112 (1977), pp. 535-542
	AQ	Blundell, T.L., et al., "Knowledge-based prediction of protein structures and the design of novel molecules", Nature, Vol. 326 (1987), pp. 347-352
ms	AR	Bowie, J., et al., "A Method to Identify Protein Sequences That Fold into a Known Three-Dimensional Structure", Science, Vol. 253 (1991), pp. 164-170

[54318-8001/LA023020.075]

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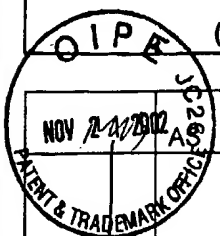
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NOV 21 2002	AS	Brenner, S., et al., "Population statistics of protein structures: lessons from structural classifications", Current Opinions on Structural Biology, Vol. 7 (1997), pp. 369-376
	AT	Brocklehurst, S., et al., "Prediction of the three-dimensional structures of the biotinylated domain from yeast pyruvate carboxylase and of the lipoylated H-protein from the pea leaf glycine cleavage system: A new automated method for prediction of protein tertiary structure", Protein Science, Vol. 2 (1993), 626-639
	AU	Browne, W.J., et al., "A Possible Three-dimensional Structure of Bovine α -Lactalbumin based on that of Hen's Egg-White Lysozyme", J. Mol. Biol., Vol. 42 (1969), pp. 65-86
	AV	Burley, S., et al., "Structural genomics: beyond the Human Genome Project", Nature Gen., Vol. 23 (1999), pp. 151-157
	AW	Classens, M., et al., "Modelling the polypeptide backbone with 'spare parts' from known protein structures", Prot. Eng., Vol. 2, No. 5 (1989), pp. 335-345
	AX	Dayhoff, M.O., et al., "A Model of Evolutionary Change in Proteins", Atlas of Prot. Seq. & Struct., Vol. 5, Supp. 3 (1979), pp. 345-352
	AY	Fischer, D., et al., "Protein fold recognition using sequence-derived predictions", Prot. Science, Vol. 5 (1996), pp. 947-955
	AZ	Gibrat, J., et al., "Surprising similarities in structure comparison", Current Opinions on Structural Biology, Vol. 7 (1996), pp. 377-385
	BA	Gotoh, O., "An Improved Algorithm for Matching Biological Sequences", J. Mol. Biol., Vol. 162 (1982), pp. 705-708
	BB	Greer, J., "Comparative Modeling Methods: Application to the Family of the Mammalian Serine Proteases", Proteins: Structure, Function & Genetics, Vol. 7 (1990), pp. 317-334
	BC	Gribskov, M., et al., "Profile Analysis", Methods of Enzymology, Vol. 183 (1990), pp. 146-159
	BD	Gribskov, M., et al., "Profile analysis: Detection of distantly related proteins", Proc. Natl. Acad. Sci. USA, Vol. 84 (1987), pp. 4355-4358
	BE	Gribskov, M., et al., "Detection of Protein Structural Features with Profile Analysis", Techniques In Protein Chemistry (1989), pp. 108-117
	BF	Havel, T.F., et al., "A New Method for Building Protein Conformations from Sequence Alignments with Homologues of Known Structure", J. Mol. Biol., Vol. 217 (1991), pp. 1-7
	BG	Heinkoff, S., et al., "Amino acid substitution matrices from protein blocks", Proc. Natl. Acad. Sci. USA, Vol. 89 (1992), pp. 10915-10919
	BH	Holm, L., et al., "Protein Structure Comparison by Alignment of Distance Matrices", J. Mol. Biol., Vol. 233 (1993), pp. 123-138
	BI	Holm, L., et al., "Mapping the Protein Universe", Science, Vol. 273, No. 5275 (1996), pp. 595-602
	BJ	Jones, T.A., et al., "Using known substructures in protein model building and crystallography", EMBO J., Vol. 5, No. (1986), pp. 819-822-
	BK	Karplus, K., et al., "Hidden Markov models for detecting remote protein homologies", Bioinformatics, Vol. 14, No. 10 (1998), pp. 846-856
	BL	Levitt, M., "Accurate Modeling of Protein Conformation by Automatic Segment Matching", J. Mol. Biol., Vol. 226 (1992), pp. 507-533
	BM	Landahl, E., et al., "Identification of Related Proteins on Family, Superfamily and Fold Level", J. Mol. Biol., Vol. 295 (2000), pp. 613-625
mm	BN	Murzin, A., et al., "SCOP: A Structural Classification of Proteins Database for the Investigation of Sequences and Structures", J. Mol. Biol., Vol. 247 (1995), pp. 536-540

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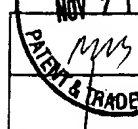
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	BO	Needleman, S., et al., "A General Method Applicable to the Search for Similarities in the Amino Acid Sequence of Two Proteins", J. Mol. Biol., Vol. 48 (1970), pp. 443-453
	BP	Rost, B., et al., "Protein Fold Recognition by Prediction-based Threading", J. Mol. Biol., Vol. 270 (1997), pp. 471-480
	BQ	Sali, A., et al., "Comparative Protein Modelling by Satisfaction of Spatial Restraints", J. Mol. Biol., Vol. 234 (1993), pp. 779-815
	BR	Sánchez, R., et al., "ModBase: A database of comparative protein structure models", Bioinformatics, Vol. 15, No. 12 (1989), pp. 1060-1061
	BS	Sánchez, R., et al., "Large-scale protein structure modeling of the <i>Saccharomyces cerevisiae</i> genome", Proc. Natl. Acad. Sci. USA, Vol. 95 (1998), pp. 13597-13602
	BT	Shindyalov, I., et al., "Protein structure alignment by incremental combinatorial extension (CE) of the optimal path", Prot. Eng., Vol. 11 (1998), pp. 739-747
	BU	Sippl, M.J., "Recognition of Errors in Three-Dimensional Structures of Proteins", Proteins: Struct, Function and Genetics, Vol. 17 (1993), pp. 355-362
	BV	Smith, T., et al., "Comparison of Biosequences", Advances in Applied Math., Vol. 2, No. 4 (1981), pp. 482-489
	BW	Smith, T., et al., "Identification of Common Molecular Subsequences", J. Mol. Biol., Vol. 147 (1981), pp. 195-197
	BX	Srinivasan, N., et al., "An evaluation of the performance of an automated procedure for comparative modeling of protein tertiary structure", Prot. Eng., Vol. 6, No. 5 (1993), pp. 501-512
	BY	Teichmann, S., et al., "Advances in structural genomics", Current Opinions on Structural Biology, Vol. 9 (1999), pp. 390-399
	BZ	Thompson, J.D., et al., "CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice", Nuc. Acids Res., Vol. 22, No. 22 (1994), pp. 4673-4680
	CA	Unger, R., et al., "A 3D Building Blocks Approach to Analyzing and Predicting Structure of Proteins", Proteins: Structure, Function, and Genetics, Vol. 5 (1989), pp. 355-373
	CB	Van Holde, K.E., "Fundamentals of X-Ray Diffraction", X-Ray Diffraction, 11 (1971), pp. 221-239
	CC	Waterman, M.S., et al., "A New Algorithm for Best Subsequence Alignments with Application to tRNA-rRNA Comparisons", J. Mol. Biol., Vol. 197 (1987), pp. 723-728

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